

R. Schwader

1644

PAGE: 1

**RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/881,509**

DATE: 04/22/1999  
TIME: 11:56:26

**INPUT SET: S31576.raw**

**This Raw Listing contains the General Information Section and those Sequences containing ERRORS.**

1 SEQUENCE LISTING

3 (1) General Information:

5 (i) APPLICANT: SCHENDEL, Dolores J.

7 (ii) TITLE OF INVENTION: T CELLS SPECIFIC FOR KIDNEY CARCINOMA

9 (iii) NUMBER OF SEQUENCES: 44

11 (iv) CORRESPONDENCE ADDRESS:

12 (A) ADDRESSEE: Nikaido, Marmelstein, Murray and Oram LLP  
13 (B) STREET: 655 15th Street, N.W., Suite 330 - G St. Lobby  
14 (C) CITY: Washington  
15 (D) STATE: DC  
16 (E) COUNTRY: USA  
17 (F) ZIP: 20005-5701

19 (vi) CURRENT APPLICATION DATA:

20 (A) APPLICATION NUMBER: 08/881,509  
21 (B) FILING DATE: June 24, 1997  
22 (C) CLASSIFICATION:

24 (viii) ATTORNEY/AGENT INFORMATION:

25 (A) NAME: Kitts, Monica Chin  
26 (B) REGISTRATION NUMBER: 36,105  
27 (C) REFERENCE/DOCKET NUMBER: 56

(ix) TELECOMMUNICATION INFORMATION:

30 (A) TELEPHONE: (202) 638-5000  
31 (B) TELEFAX: (202) 638-4810

*Does Not Comply  
Corrected Diskette Needed*

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE:  
(B) COMPUTER:  
(C) OPERATING SYSTEM:  
(D) SOFTWARE:

add these  
Mandatory headings  
and responses for a  
U.S. case

## **ERRORED SEQUENCES FOLLOW:**

204 (2) INFORMATION FOR SEQ ID NO: 3:

205

206 (i) SEQUENCE CHARACTERISTICS:

207

208

209

210

- (A) LENGTH: 936 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(next page)

**RAW SEQUENCE LISTING  
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211
212     (ix) FEATURE:
213         (A) NAME/KEY: CDS
214         (B) LOCATION:1..933
215
216     (ix) FEATURE:
217         (A) NAME/KEY: sig_peptide
218         (B) LOCATION:1..63
219
220     (ix) FEATURE:
221         (A) NAME/KEY: mat_peptide
222         (B) LOCATION:64..933
223
224     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
225
226 ATG GAT ACC TGG CTC GTA TGC TGG GCA ATT TTT AGT CTC TTG AAA GCA      48
227 Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala
228 -21 -20           -15           -10
229
230 GGA CTC ACA GAA CCT GAA GTC ACC CAG ACT CCC AGC CAT CAG GTC ACA      96
231 Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr
232 -5             1             5             10
233
234 CAG ATG GGA CAG GAA GTG ATC TTG CGC TGT GTC CCC ATC TCT AAT CAC      144
235 Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His
236   15            20            25
237
238 TTA TAC TTC TAT TGG TAC AGA CAA ATC TTG GGG CAG AAA GTC GAG TTT      192
239 Leu Tyr Phe Tyr Trp Tyr Arg Gln Ile Leu Gly Gln Lys Val Glu Phe
240   30            35            40
241
242 CTG GTT TCC TTT TAT AAT AAT GAA ATC TCA GAG AAG TCT GAA ATA TTC      240
243 Leu Val Ser Phe Tyr Asn Asn Glu Ile Ser Glu Lys Ser Glu Ile Phe
244   45            50            55
245
246 GAT GAT CAA TTC TCA GTT GAA AGG CCT GAT GGA TCA AAT TTC ACT CTG      288
247
248 Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu      288
249   60            65            70            75
250
--> 251 AAG ATC CGG TCC ACA AAG CTG GAG GAC TCA GCC ATG TAC TTC TGT GCC      336 OK
252 Lys Ile Arg Ser Thr Lys Leu Glu Asp Ser Ala Met Tyr Phe Cys Ala
253   80            85            90
254
255 AGC AGC GAA ACT AAC TCC TAC GAG CAG TAC TTC GGG CCG GGC ACC AGG      384
256 Ser Ser Glu Thr Asn Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg
257   95            100           105
258
259 CTC ACG GTC ACA GAG GAC CTG AAA AAC GTG TTC CCA CCC GAG GTC GCT      432
260 Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
261   110           115           120
262
263 GTG TTT GAG CCA TCA GAA GCA GAG ATC TCC CAC ACC CAA AAG GCC ACA      480

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288  
mat my

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**RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/881,509**

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|     |   |     |     |     |
|-----|---|-----|-----|-----|
| 264 | Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr |     |     |     |
| 265 | 125   | 130 | 135 |     |
| 266 |   |     |     |     |
| 267 | CTG GTG TGC CTG GCC ACA GGC TTC TAC CCC GAC CAC GTG GAG CTG AGC | 528 |     |     |
| 268 | Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser |     |     |     |
| 269 | 140   | 145 | 150 | 155 |
| 270 |   |     |     |     |
| 271 | TGG TGG GTG AAT GGG AAG GAG GTG CAC AGT GGG GTC AGC ACA GAC CCG | 576 |     |     |
| 272 | Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro |     |     |     |
| 273 | 160   | 165 | 170 |     |

Please ignore  
Mark Martin

08/881,809

274  
275 CAG CCC CTC AAG GAG CAG CCC GCC CTC AAT GAC TCC AGA TAC TGC CTG 624  
276 Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu  
277 175 180 185  
278  
279 AGC AGC CGC CTG AGG GTC TCG GCC ACC TTC TGG CAG AAC CCC CGC AAC 672  
280 Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn  
281 190 195 200  
282  
283 CAC TTC CGC TGT CAA GTC CAG TTC TAC GGG CTC TCG GAG AAT GAC GAG 720  
284 His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu  
285 205 210 215  
286  
287 TGG ACC CAG GAT AGG GCC AAA CCT GTC ACC CAG ATC GTC AGC GCC GAG 768  
288 Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu  
289 220 225 230 235  
290  
291 GCC TGG GGT AGA GCA GAC TGT GGC TTC ACC TCC GAG TCT TAC CAG CAA 816  
292 Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln  
293 240 245 250  
294  
295 GGG GTC CTG TCT GCC ACC ATC CTC TAT GAG ATC TTG CTA GGG AAG GCC 864  
296 Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala  
297 255 260 265  
298  
299 ACC TTG TAT GCC GTG CTG GTC AGT GCC CTC GTG CTG ATG GCC ATG GTC 912  
300 Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val  
301 270 275 280  
302  
303 AAG AGA AAG GAT TCC AGA GGC TAG 936  
304 Lys Arg Lys Asp Ser Arg Gly  
305 285 290  
306  
307

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654 (2) INFORMATION FOR SEQ ID NO: 22:

655

656 (i) SEQUENCE CHARACTERISTICS:

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- 657 (A) LENGTH: 20 base pairs
- 658 (B) TYPE: nucleic acid
- 659 (C) STRANDEDNESS: single
- 660 (D) TOPOLOGY: linear

*next page*

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RAW SEQUENCE LISTING  
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662 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
663  
664 TAGAGGATGG TGGCAGACAG  
665  
666

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20 - insert  
cumulative  
base total  
at right  
margin

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/881,509**

DATE: 04/22/1999  
TIME: 11:56:27

**INPUT SET: S31576.raw**

| Line | Error  | Original Text                              |
|------|--|--|
| 207  | Entered (936) and Calc. Seq. Length (888) differ   | (A) LENGTH: 936 base pairs                 |
| 251  | # of Sequences for line conflicts w/ running total | AAG ATC CGG TCC ACA AAG CTG GAG GAC TCA GC |
| 657  | Entered (20) and Calc. Seq. Length (0) differ      | (A) LENGTH: 20 base pairs                  |

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**SEQUENCE MISSING ITEM REPORT**  
**PATENT APPLICATION US/08/881,509**

DATE: 04/22/1999  
TIME: 11:56:27

***INPUT SET: S31576.raw***

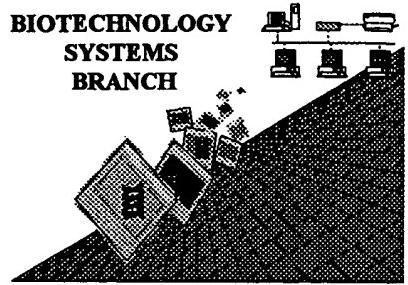
MEDIUM TYPE  
COMPUTER  
OPERATING SYSTEM  
SOFTWARE  
COMPUTER READABLE FORM  
APPLICATION NUMBER  
FILING DATE  
PRIOR APPLICATION DATA

Schwadron

# RAW SEQUENCE LISTING

## ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:**

Application Serial Number: 08/881,509

Art Unit / Team No.: 1644

Date Processed by STIC: 4/22/99

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

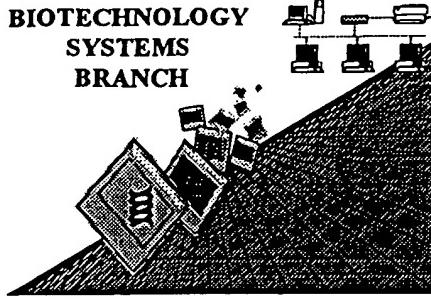
**1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**

**2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**ARTI SHAH 703-308-4212**



## Notice of Availability of Checker Program

### Applicant Aid for Biotechnology Computer Readable Form (CRF) Sequence Listing Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (Sequence Rules: 37CRF 1.821 through 1.825).

Final rules were published in the *Federal Register* (55 FR18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software is available via computer downloading, details are below. Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the PTO *Official Gazette*.

The software can be accessed/requested from the following locations:

- 1) Dial-up access through the Internet. Location is <ftp://ftp.uspto.gov>  
The software is in current directory: pub/checker/  
Download all the files. Cost: Free-of-charge
- 3) For diskette copies, mail to: U.S.P.T.O., OEIP, CRYSTAL PARK 3, SUITE 441  
WASHINGTON DC 20231

**COST FOR DISKETTE IS \$ 25.00**

**METHOD OF PAYMENT:**

Check payable to Commissioner of Patents and Trademarks  
VISA/ Mastercard/ Charge- Charges can be faxed to 703-306-2737  
PTO Deposit Account

*For Further Information, Contact: Arti Shah at 703-308-4212*

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
7. Other: \_\_\_\_\_

**Applicant Must Provide:**

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216  
For CRF Submission Help, call (703) 308-4212  
For PatentIn software help, call (703) 308-6856

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